

1632

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See page 6



1600

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/812,350

DATE: 09/10/2002  
 TIME: 15:35:53

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SEP 24 2002

Input Set : A:\P01979US2.txt  
 Output Set: N:\CRF4\09102002\I812350.raw

TECH CENTER 1600/2900

3 <110> APPLICANT: Lindquist, Susan  
 4 Queitsch, Christine  
 5 Vierling, Elizabeth  
 7 <120> TITLE OF INVENTION: Transgenic Plants Containing Heat Shock Protein  
 9 <130> FILE REFERENCE: P01979US2  
 11 <140> CURRENT APPLICATION NUMBER: US 09/812,350  
 12 <141> CURRENT FILING DATE: 2001-03-20  
 14 <150> PRIOR APPLICATION NUMBER: US 60/190,769  
 15 <151> PRIOR FILING DATE: 2000-03-20  
 17 <150> PRIOR APPLICATION NUMBER: US 60/198,116  
 18 <151> PRIOR FILING DATE: 2000-04-18  
 20 <160> NUMBER OF SEQ ID NOS: 49  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 883  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Synechococcus  
 29 <400> SEQUENCE: 1  
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 36 20 25 30  
 39 Ala Lys Gln Ala Gln His Gln Gln Ile Glu Ser Glu His Leu Phe Leu  
 40 35 40 45  
 43 Ala Leu Leu Gln Glu Pro Gly Leu Ala Leu Asn Ile Leu Lys Lys Ala  
 44 50 55 60  
 47 Gly Leu Glu Ala Ala Gln Leu Gln Gln Phe Thr Glu Arg Phe Ile Ala  
 48 65 70 75 80  
 51 Arg Gln Pro Lys Val Ser Gly Gly Asn Gln Ser Val Tyr Leu Gly Arg  
 52 85 90 95  
 55 Ser Leu Asp Gln Leu Leu Asp Gln Ala Asp Gln Phe Arg Lys Asp Phe  
 56 100 105 110  
 59 Gly Asp Glu Phe Ile Ser Val Glu His Leu Ile Leu Ser Phe Pro Arg  
 60 115 120 125  
 63 Asp Ser Arg Phe Gly Arg Leu Leu Ser Gln Glu Phe Lys Val Asp Glu  
 64 130 135 140  
 67 Lys Gln Leu Arg Gln Ile Ile Gln Gln Ile Arg Gly Ser Gln Lys Val  
 68 145 150 155 160  
 71 Thr Asp Gln Asn Pro Glu Gly Lys Tyr Glu Ala Leu Glu Lys Tyr Gly  
 72 165 170 175  
 75 Arg Asp Leu Thr Glu Met Ala Arg Arg Gly Lys Leu Asp Pro Val Ile  
 76 180 185 190  
 79 Gly Arg Asp Asp Glu Ile Arg Arg Thr Ile Gln Ile Leu Ser Arg Arg

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83 Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys Thr
84      210          215          220
87 Ala Ile Ala Glu Gly Leu Ala Gln Arg Ile Ile Asn Gly Asp Val Pro
88 225          230          235          240
91 Gln Ser Leu Lys Asp Arg Arg Leu Ile Ala Leu Asp Met Gly Ala Leu
92      245          250          255
95 Ile Ala Gly Ala Lys Phe Arg Gly Glu Phe Glu Glu Arg Leu Thr Ala
96      260          265          270
99 Val Leu Lys Glu Val Thr Asp Ser Glu Gly Ile Ile Ile Leu Phe Ile
100     275          280          285
103 Asp Glu Met His Thr Val Val Gly Ala Gly Ala Val Gln Gly Ser Met
104     290          295          300
107 Asp Ala Gly Asn Leu Leu Lys Thr Met Leu Ala Arg Gly Glu Leu Arg
108 305          310          315          320
111 Cys Ile Gly Ala Thr Thr Leu Gly Lys Tyr Arg Gln Tyr Ile Glu Lys
112     325          330          335
115 Asp Ala Ala Leu Glu Arg Arg Phe Gln Gln Val Phe Val Asp Gln Pro
116     340          345          350
119 Thr Val Glu Asp Thr Ile Ser Ile Leu Arg Gly Leu Lys Glu Arg Tyr
120     355          360          365
123 Glu Val His His Gly Val Arg Ile Ser Asp Asn Ala Leu Val Ala Ala
124     370          375          380
127 Ala Val Leu Ser Thr Arg Tyr Ile Ser Asp Arg Phe Leu Pro Asp Lys
128 385          390          395          400
131 Ala Ile Asp Leu Val Asp Glu Ser Ala Ala Arg Leu Lys Met Glu Ile
132     405          410          415
135 Thr Ser Lys Pro Glu Glu Leu Asp Glu Ile Asp Arg Lys Ile Leu Gln
136     420          425          430
139 Leu Glu Met Glu Arg Leu Ser Leu Gln Lys Glu Ser Asp Leu Ala Ser
140     435          440          445
143 Gln Glu Arg Leu Gln Arg Leu Glu Lys Glu Leu Ala Asp Leu Lys Glu
144     450          455          460
147 Glu Gln Arg Ser Leu Ser Ser Gln Trp Gln Ala Glu Lys Asp Val Ile
148 465          470          475          480
151 Thr Asp Ile Gln Ser Val Lys Glu Glu Ile Asp Gln Val Asn Leu Leu
152     485          490          495
155 Ile Gln Gln Ala Glu Arg Asp Tyr Asp Leu Asn Lys Ala Ala Glu Leu
156     500          505          510
159 Lys Tyr Gly Lys Leu Thr Glu Leu Gln Arg Lys Leu Asn Glu Met Glu
160     515          520          525
163 Gly Gly Leu Ala Thr Thr His Thr Ser Gly Lys Ser Leu Leu Arg Glu
164     530          535          540
167 Glu Val Thr Glu Val Asp Ile Ala Glu Ile Ile Ser Lys Trp Thr Gly
168 545          550          555          560
171 Ile Pro Val Ser Lys Leu Val Glu Ser Glu Met Gln Lys Leu Leu Asn
172     565          570          575
175 Leu Asp Glu Glu Leu His Gln Arg Val Ile Gly Gln Glu Glu Ala Val
176     580          585          590

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179 Ser Ala Val Ala Asp Ala Ile Gln Arg Ser Arg Ala Gly Leu Ser Asp
180      595      600      605
183 Pro Lys Arg Pro Ile Ala Ser Phe Ile Phe Leu Gly Pro Thr Gly Val
184      610      615      620
187 Gly Lys Thr Glu Leu Ala Lys Ala Leu Ala Ala Tyr Leu Phe Asp Thr
188 625      630      635      640
191 Glu Asp Ala Met Ile Arg Ile Asp Met Ser Glu Tyr Met Glu Lys His
192      645      650      655
195 Ala Val Ser Arg Leu Ile Gly Ala Pro Gly Tyr Val Gly Tyr Asp
196      660      665      670
199 Glu Gly Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Ser Val
200      675      680      685
203 Ile Leu Phe Asp Glu Ile Glu Lys Ala His Pro Asp Val Phe Asn Val
204      690      695      700
207 Met Leu Gln Ile Leu Asp Asp Gly Arg Val Thr Asp Ser Arg Gly Arg
208 705      710      715      720
211 Thr Val Asp Phe Lys Asn Thr Ile Leu Ile Leu Thr Ser Asn Ile Gly
212      725      730      735
215 Ser Gln Tyr Ile Leu Asp Val Ala Gly Asp Asp Ser Arg Tyr Glu Glu
216      740      745      750
219 Met Arg Ser Arg Val Thr Glu Ala Leu Arg Ala Asn Phe Arg Pro Glu
220      755      760      765
223 Phe Leu Asn Arg Val Asp Glu Thr Ile Ile Phe His Ser Leu Arg Lys
224      770      775      780
227 Asp Gln Leu Gln Gln Ile Val Arg Ile Gln Leu His Arg Leu Glu Glu
228 785      790      795      800
231 Arg Leu Ser Asp Arg Lys Leu Ser Leu Ser Met Ser Pro Glu Ala Ile
232      805      810      815
235 Asp Phe Leu Val Glu Ile Gly Phe Asp Pro Val Tyr Gly Ala Arg Pro
236      820      825      830
239 Leu Lys Arg Val Ile Gln Arg Glu Leu Glu Thr Ala Ile Ala Lys Ala
240      835      840      845
243 Ile Leu Arg Gly Gln Phe Ser Asp Gly Asp Thr Ile Gln Val Ala Val
244      850      855      860
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248 865      870      875      880
251 Pro Leu Ser
255 <210> SEQ ID NO: 2
256 <211> LENGTH: 856
257 <212> TYPE: PRT
258 <213> ORGANISM: Helicobacter pylori
260 <400> SEQUENCE: 2
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266 Ser Ala Leu Ala Leu Ala Leu His His Lys Asn Ala Glu Val Thr Pro
267      20      25      30
270 Leu His Met Leu Phe Ala Met Leu Asn Asn Ser Gln Gly Ile Leu Ile
271      35      40      45
274 Gln Ala Leu Gln Lys Met Pro Val Asp Ile Glu Ala Leu Lys Leu Ser

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275	50				55				60										
278	Val	Gln	Ser	Glu	Leu	Asn	Lys	Phe	Ala	Lys	Val	Ser	Gln	Ile	Asn	Lys			
279	65					70					75				80				
282	Gln	Asn	Ile	Gln	Leu	Asn	Gln	Ala	Leu	Ile	Gln	Ser	Leu	Glu	Asn	Ala			
283					85						90				95				
286	Gln	Gly	Leu	Met	Ala	Lys	Thr	Gly	Asp	Ser	Phe	Ile	Ala	Thr	Asp	Val			
287				100					105					110					
290	Tyr	Leu	Leu	Ala	Asn	Met	Ser	Leu	Phe	Glu	Ser	Val	Leu	Lys	Pro	Tyr			
291			115					120					125						
294	Leu	Asp	Thr	Lys	Glu	Leu	Gln	Lys	Thr	Leu	Glu	Ser	Leu	Arg	Lys	Gly			
295			130					135					140						
298	Ala	Thr	Ile	Gln	Gly	Lys	Asn	Asp	Asp	Ser	Asn	Leu	Glu	Ser	Leu	Glu			
299	145					150					155				160				
302	Lys	Phe	Gly	Ile	Asp	Leu	Thr	Gln	Lys	Ala	Leu	Glu	Asn	Lys	Leu	Asp			
303					165					170					175				
306	Pro	Val	Ile	Gly	Arg	Asp	Glu	Glu	Ile	Ile	Arg	Met	Met	Gln	Ile	Leu			
307				180					185					190					
310	Ile	Arg	Lys	Thr	Lys	Asn	Asn	Pro	Ile	Leu	Leu	Gly	Glu	Pro	Gly	Val			
311				195				200					205						
314	Gly	Lys	Thr	Ala	Val	Val	Glu	Gly	Leu	Ala	Gln	Arg	Ile	Val	Asn	Lys			
315			210				215					220							
318	Glu	Val	Pro	Lys	Thr	Leu	Leu	Asn	Lys	Arg	Val	Ile	Ala	Leu	Asp	Leu			
319	225					230					235				240				
322	Ser	Leu	Leu	Val	Ala	Gly	Ala	Lys	Tyr	Arg	Gly	Glu	Phe	Glu	Glu	Arg			
323					245					250					255				
326	Leu	Lys	Lys	Val	Ile	Glu	Glu	Val	Lys	Lys	Ser	Ala	Asn	Val	Ile	Leu			
327				260					265					270					
330	Phe	Ile	Asp	Glu	Ile	His	Thr	Ile	Val	Gly	Ala	Gly	Ala	Ser	Glu	Gly			
331				275				280					285						
334	Gly	Met	Asp	Ala	Ala	Asn	Ile	Leu	Lys	Pro	Ala	Leu	Ala	Arg	Gly	Glu			
335			290				295					300							
338	Leu	His	Thr	Ile	Gly	Ala	Thr	Thr	Leu	Lys	Glu	Tyr	Arg	Lys	Tyr	Phe			
339	305					310						315			320				
342	Glu	Lys	Asp	Met	Ala	Leu	Gln	Arg	Arg	Phe	Gln	Pro	Ile	Leu	Leu	Asn			
343					325					330					335				
346	Glu	Pro	Ser	Ile	Asn	Glu	Ala	Leu	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Glu			
347					340					345					350				
350	Thr	Leu	Glu	Thr	His	His	Asn	Ile	Thr	Ile	Asn	Asp	Ser	Ala	Leu	Ile			
351				355				360					365						
354	Ala	Ser	Ala	Lys	Leu	Ser	Ser	Arg	Tyr	Ile	Thr	Asp	Arg	Phe	Leu	Pro			
355				370				375					380						
358	Asp	Lys	Ala	Ile	Asp	Leu	Ile	Asp	Glu	Gly	Ala	Ala	Gln	Leu	Lys	Met			
359	385					390						395			400				
362	Gln	Met	Glu	Ser	Glu	Pro	Ala	Lys	Leu	Ser	Ser	Val	Lys	Arg	Ser	Ile			
363					405					410					415				
366	Gln	Arg	Leu	Glu	Met	Glu	Lys	Gln	Ala	Leu	Glu	Met	Glu	Lys	Lys	Glu			
367					420					425					430				
370	Ser	Asn	His	Lys	Arg	Met	Gln	Glu	Ile	Leu	Lys	Glu	Leu	Ser	Asp	Leu			
371				435				440							445				

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374 Lys Glu Glu Lys Ile Gln Leu Glu Ala Gln Phe Glu Asn Glu Lys Glu
375      450      455      460
378 Ala Phe Lys Glu Ile Ser Arg Leu Lys Met Glu Met Glu Ser Leu Lys
379 465      470      475      480
382 Lys Glu Ala Glu Arg Phe Lys Arg Asn Gly Asp Tyr Gln Gln Ala Gly
383      485      490      495
386 Glu Ile Glu Tyr Ser Lys Ile Pro Glu Asn Lys Lys Lys Glu Glu Glu
387      500      505      510
390 Leu Gln Arg Lys Trp Glu Ala Met Gln Gln Asn Gly Ala Leu Leu Gln
391      515      520      525
394 Asn Ala Leu Thr Glu Asn Asn Ile Ala Glu Ile Val Ser Gln Trp Thr
395      530      535      540
398 His Ile Pro Val Gln Lys Met Leu Gln Ser Glu Lys Asn Arg Val Leu
399 545      550      555      560
402 Asn Ile Glu Ser Glu Leu Gln Lys Arg Val Val Gly Gln Glu Lys Ala
403      565      570      575
406 Ile Lys Ala Ile Ala Lys Ala Ile Lys Arg Asn Lys Ala Gly Leu Ser
407      580      585      590
410 Asp Ser Asn Lys Pro Ile Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly
411      595      600      605
414 Val Gly Lys Thr Glu Ser Ala Lys Ala Leu Ala Gln Phe Leu Phe Asp
415      610      615      620
418 Ser Asp Lys Asn Leu Ile Arg Ile Asp Met Ser Glu Tyr Leu Glu Lys
419 625      630      635      640
422 His Ala Ile Thr Arg Leu Ile Gly Pro Ala Pro Gly Tyr Val Gly Tyr
423      645      650      655
426 Glu Glu Gly Gly Gln Leu Thr Glu Ala Val Arg Arg Lys Pro Tyr Ser
427      660      665      670
430 Val Val Leu Leu Asp Glu Val Glu Lys Ala His Pro Asp Val Phe Asn
431      675      680      685
434 Leu Leu Leu Gln Val Leu Asp Glu Gly His Leu Thr Asp Ser Lys Gly
435      690      695      700
438 Val Arg Val Asp Phe Lys Asn Thr Ile Leu Ile Leu Thr Ser Asn Val
439 705      710      715      720
442 Ala Ser Gly Ala Leu Leu Glu Glu Asn Leu Ser Glu Ala Asp Lys Gln
443      725      730      735
446 Lys Ala Ile Lys Glu Ser Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu
447      740      745      750
450 Asn Arg Leu Asp Glu Ile Ile Ser Phe Asn Ala Leu Gly Ser His Ala
451      755      760      765
454 Val Ile Asn Ile Val Gly Ile Leu Phe Glu Asn Ile Gln Lys Lys Ala
455      770      775      780
458 Leu Glu Arg Gly Ile Asn Ile Thr Leu Asp Glu Glu Ala Lys Glu Leu
459 785      790      795      800
462 Ile Ala Glu Ala Gly Phe Asp Arg Phe Tyr Gly Ala Arg Pro Leu Lys
463      805      810      815
466 Arg Ala Leu Tyr Glu Met Val Glu Asp Lys Leu Ala Glu Leu Ile Leu
467      820      825      830
470 Glu Asp Lys Ile Lys Glu Asn Gly Ser Val Ala Phe Val Val Glu Asn

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; N Pos. 3710

VERIFICATION SUMMARY

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Input Set : A:\P01979US2.txt

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L:6356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:3660